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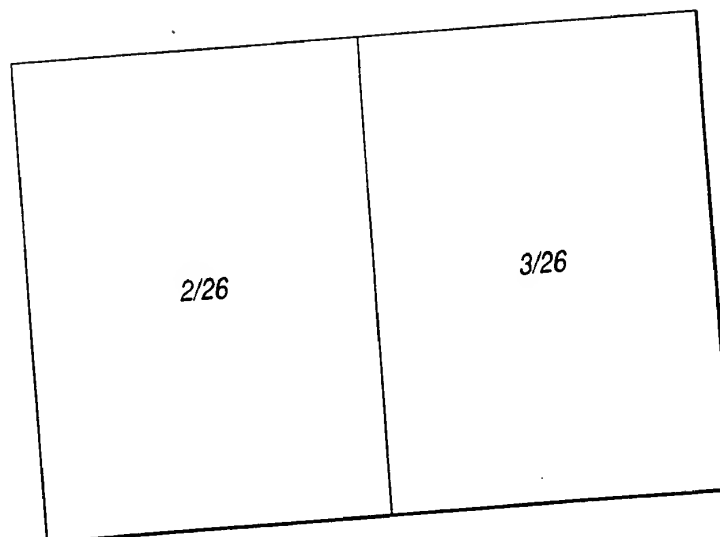


Fig. 1

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	A	S1
Bclw	MATPASTPDT	RALVADFVGY
Bclw-Rox	MATPASTPDT	RALVADFVGY
Bclw	DEFETRFRRT	FSDLAAQLHV
Bclw-Rox	DEFETRFRRT	FSDLAAQLHV
Bclw	VFGAALCAES	VNKEMEPLVG
Bclw-Rox	VFGAALCAES	VNKEMEPLVG
Bclw	YGDGALEEAR	RLREGNWASV
Bclw-Rox	ARVREMEEEA	EKLKELQNEV
Bclw-Rox	IYVGNVDYGA	TAELEAHFH
Bclw-Rox	ESVRTSLALD	ESLFRGRQIK
Bclw-Rox	NSSRSRFYSG	FNSRPRGRIY

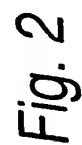
Fig. 1 (i)

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PCT/AU97/00199

KLRQKGYVCG	AGPGEGPAAD	PLHQAMRAAG	50		
KLRQKGYVCG	AGPGEGPAAD	PLHQAMRAAG	50		
S2					
TPGSAQQRFT	QVSDELFQGG	PNWGRLVAFF	100		
TPGSAQQRFT	QVSDELFQGG	PNWGRLVAFF	100		
S3					
E	QVQDWMVAYL	ETRLADWIHS	SGGWAEFTAL	150	
	QVQDWMVAYL	ETRLADWIHS	SGGW <sup>▲</sup> ELEAIK	150	
RTVLTGAVAL			GALVTVGAFF	ASK*	193
EKQMNMSPPP			GNAGPVIMSL	EEKMEADARS	200
GCGSVNRVTI			LCDKFSGHPK	GFAYIEFSDK	250
VIPKRTNRPG			ISTTDRGFPR	SRYRARTTNY	300
RGRARATSWY			SPY*		333

Fig. 1 (ii)



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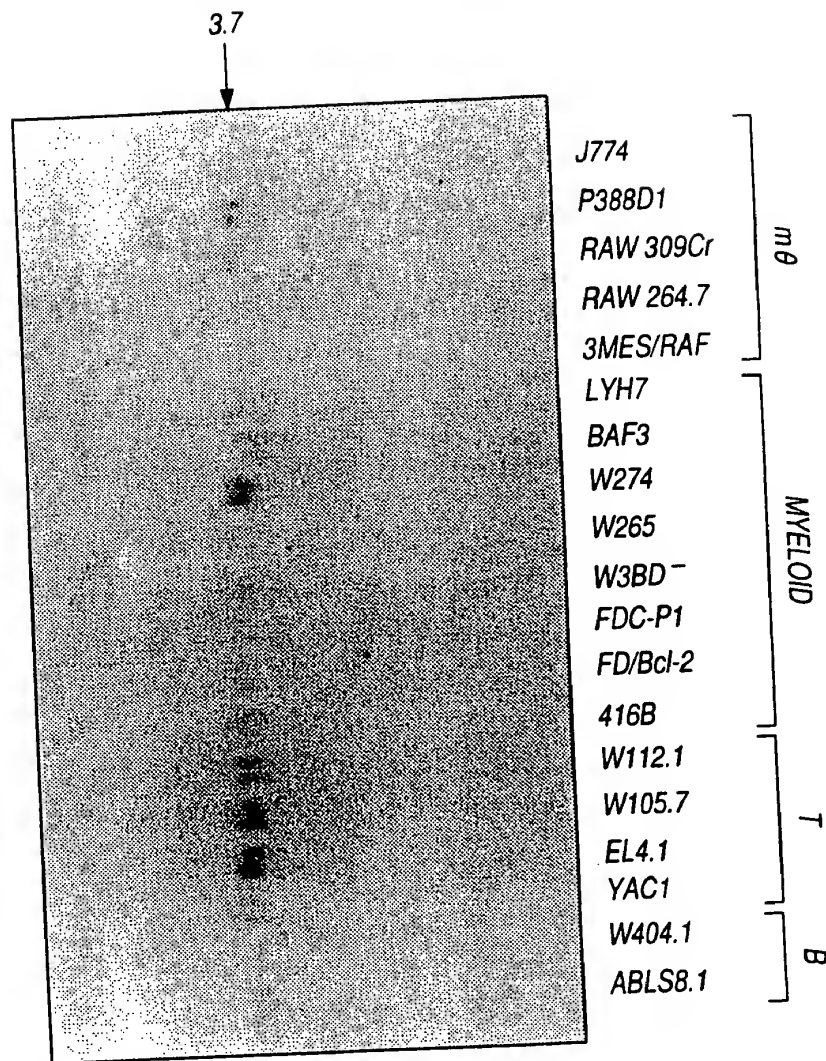


Fig. 3

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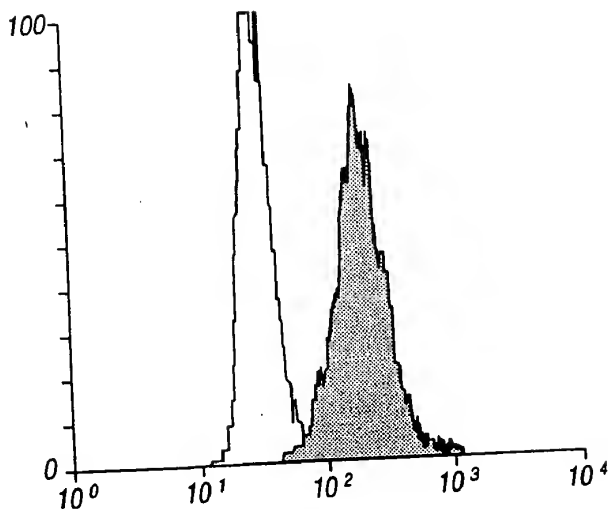


Fig. 4A

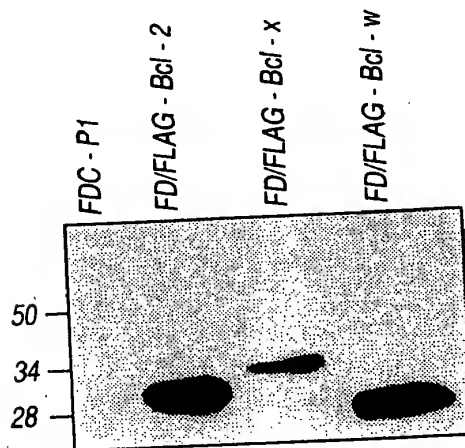


Fig. 4B

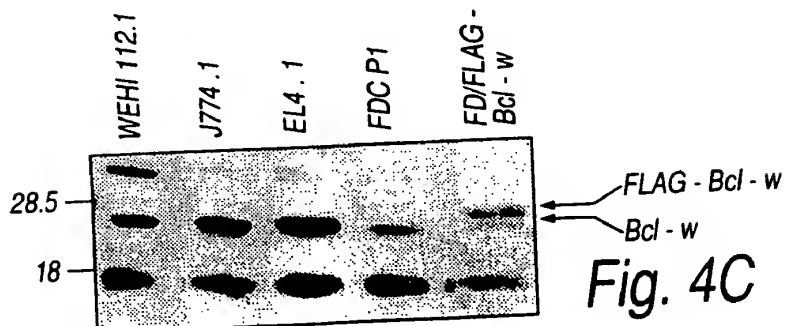


Fig. 4C

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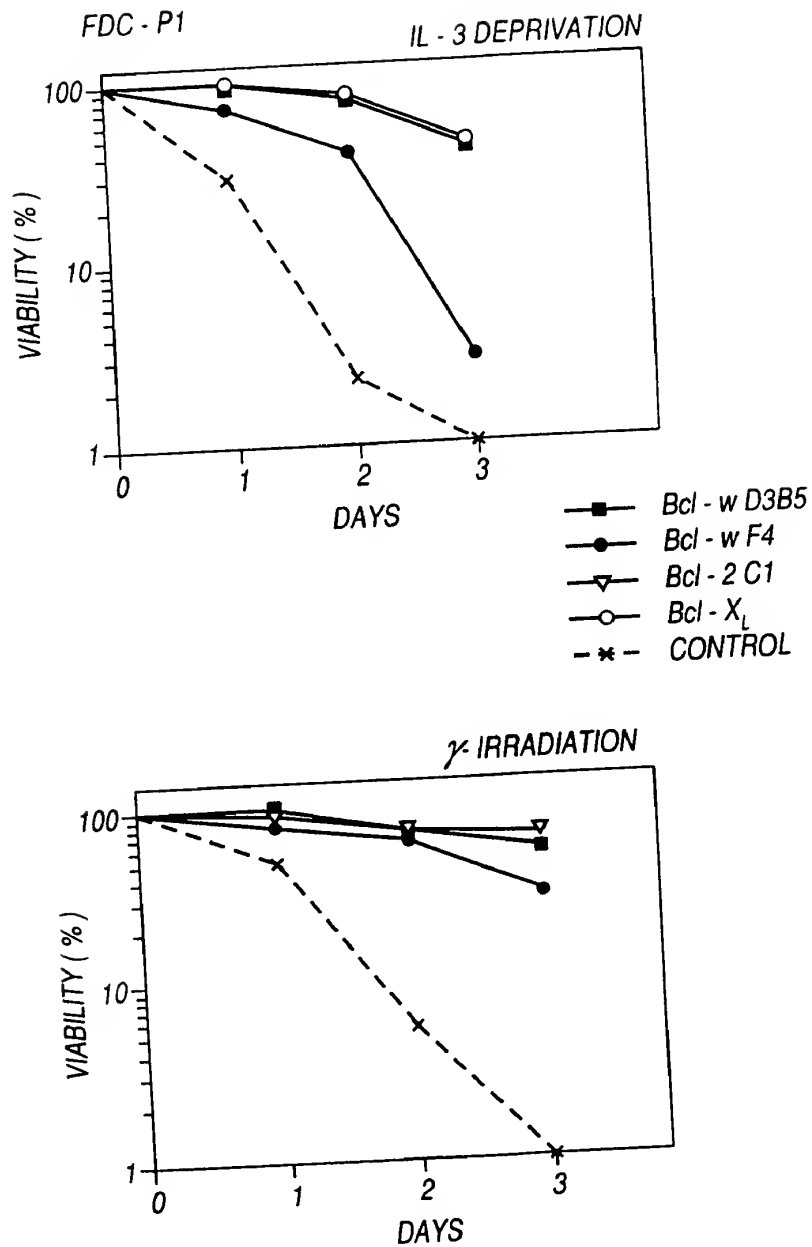


Fig. 5A

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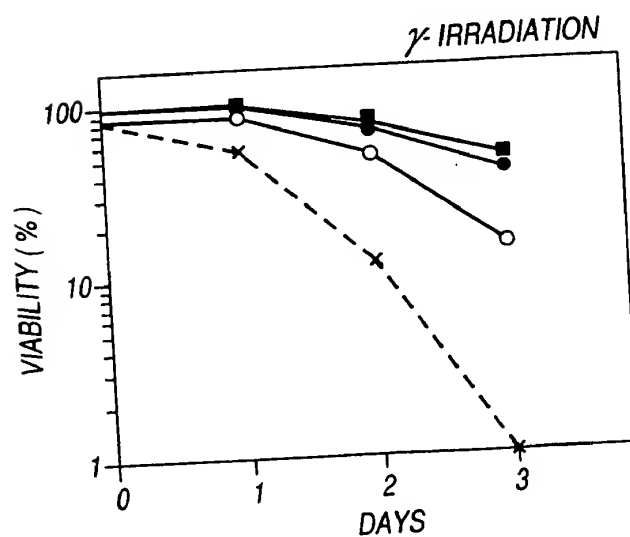
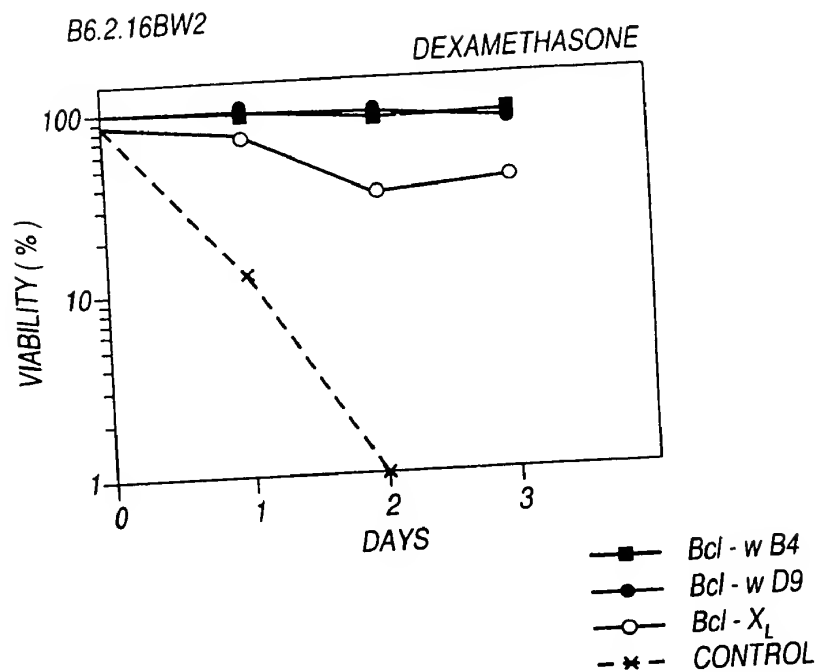


Fig. 5B

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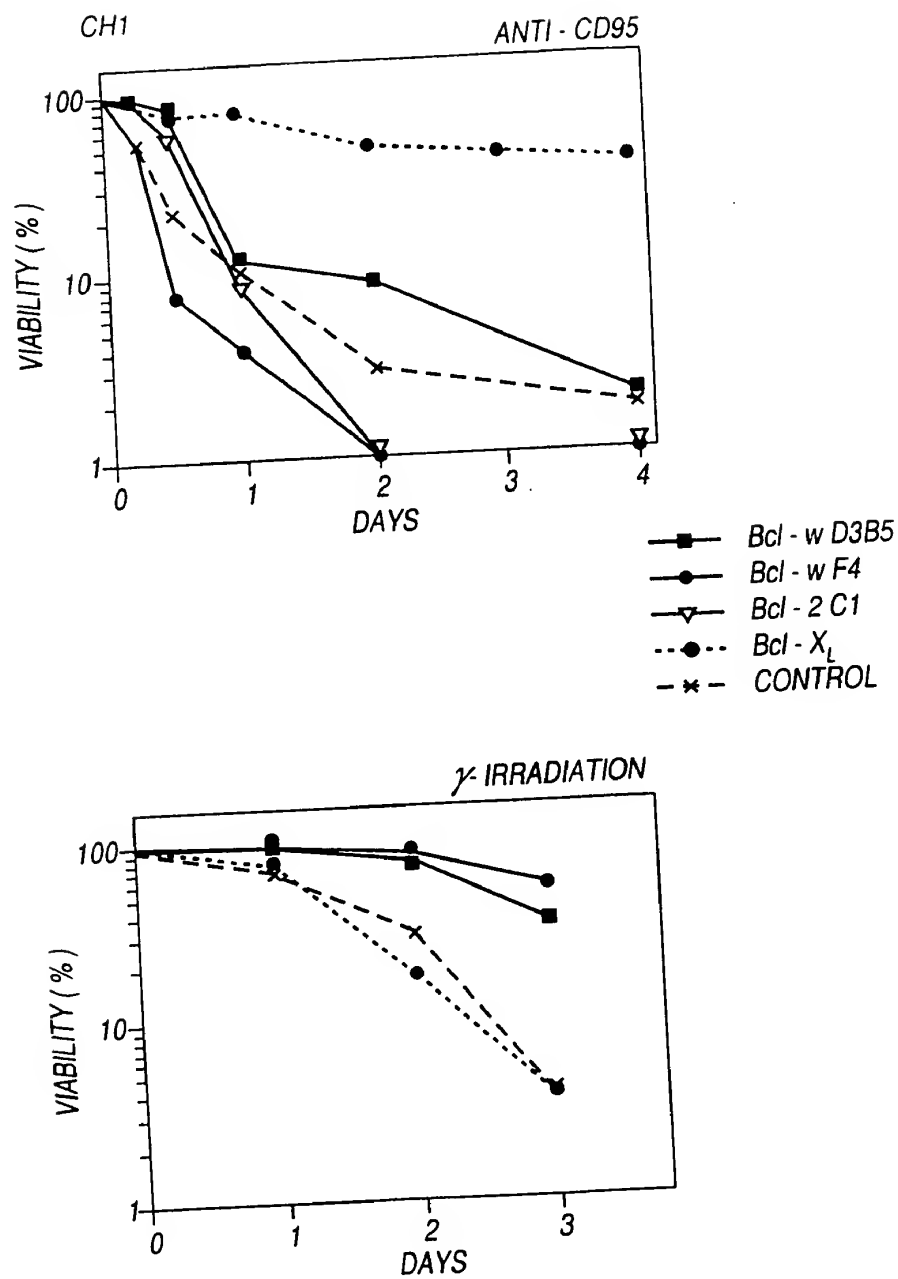


































Fig. 5C

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<i>Sftp1</i>								
<i>Tcra</i>								
<i>Bclw</i>								
<i>Gja3</i>								
	59	62	3	8	0	1	1	0

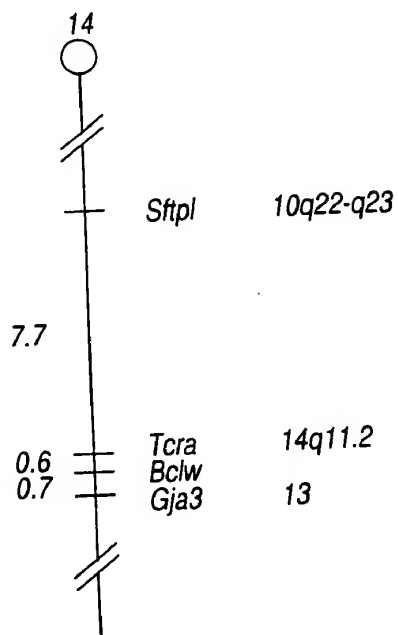


Fig. 6

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Fig. 7A



Fig. 7B

- 12/26

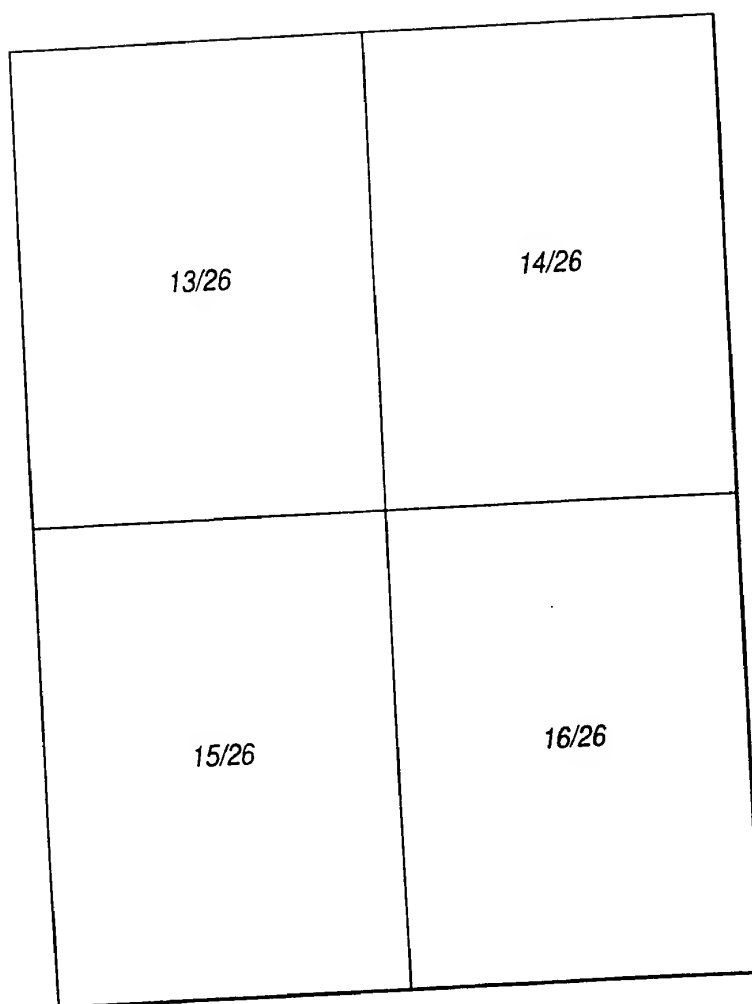


Fig. 8

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S1

Bc12	MAHAGRTGYD	NREI VMKYIH	YKLSORGYEW
Bc1x <sub>L</sub>	.....MSQS	NRELVVDFLS	YKLSOKGYSW
Bc1w	.MATPASAPD	TRALVADFGV	YKLRKGYVC
Ced9		D IEGFVVDYFT	HRIRONGMEW

MASG

Bak

Bax

Bc12	ASRDPVARTS	PLQTPAAPGA	AAGPAL....
Bc1x <sub>L</sub>	PSWH.LADSP	AVNGATGHSS	SLDARE....
Bc1w	.....	.....	.....
Ced9			

Bak	FRSYVFYRHQ	QEQEAEGVAA	PADPEMVTLP
Bax	....ALLQG	FIQDRAGRMG	GEAPELALDP
Bik			

S2

Bc12	MSROLHLTP	FTARGREATV	VEELERDG.V
Bc1x <sub>L</sub>	LTSQLHITP	GTAYQSEEQV	VNELERDG.V
Bc1w	LAAQLHVTP	GSAQQRETQV	SDELFQGG.P
CED9	FCEQLLAVP	RISFSLYQDV	VRTVGNAQTD

Fig. 8 (i)

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BH3

NH1

\* \*

△

BH1

	*NWGRIV	AFFFEFGG..V	.MCVESVNRE	165
....	NWGRIV	AFFSFGG..A	.LCVESVDKE	158
....	NWGRIV	AFFSFGG..A	.LCAESVNKE	114
....	NWGRLV	AFFEVEGA..A	.AKMMESV..E	190
OCPMSYGRLI	GLISFEGGFVA			

Fig. 8 ( ii )

WO 97/35971

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Bak	MLQHLOPTA	ENAYEYETKI	ATSLFESG. I
Bax	MIAAVD..T	DSPREVEFRV	AADMESDGNF

S3

Bc12	MSPLVDNTAL	WMTEYLNHRH.	LHTWIQDNGG
Bc1x <sub>L</sub>	MOVLVSRIAA	WMATYLNDRH.	LEPWIQENGG
Bc1w	MEPLVGQVQE	WMVAYLETR.	LADWTHSSGG
Ced9	LOGQVRNLFV	YTSLFIKTRI	RNNWKEHNRS

Bak	LTGFLGQVTR	FVVDFMLHHC	IARWIAQRGG
Bax	VPELIRTIMG	WTLDFLRERL	LG.WIQDQGG

Bc12	DFSWLSLKT	LSLAL.VGAC	ITLGAYLGHK
Bc1x <sub>L</sub>	RKGQERFNRW	FLTGMTVAGV	VLLGSLFSRK
Bc1w	EGNWASVRTV	LTGAVALGAL	VTVGAFASK

Bak	.....GP	ILNVLVVLGV	VLLGQFVVR
Bax	.....TPT	WQTVTIFVAG	VTASLTIWK

Fig. 8 ( iii )

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....NWGRVV	ALLGEGY..R	..LALHVVYQHG	146
....NWGRVV	ALFYFAS..K	..LVLKALCTK	128
	△		
BH2			
WDAFVELYG.	...PSMRPLF		210
WDTFVELYG.	...NNAAAES		203
WAEFTALYGD	GALEEARRLR		163
WDDFMTL.G.			218
WVAALNLGN.	.....		185
WDGLLSYFG.	.....		166
			239
			233
			193
FFKS			211
KMG			192

Fig. 8 (iv)

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20/26	21/26

Fig. 9A

18/26

ATG GCG ACC CCA GCC TCG GCC CCA GAC  
Met Ala Thr Pro Ala Ser Ala Pro Asp  
1 5

TTT GTA GGT TAT AAG CTG AGG CAG AAG  
Phe Val Gly Tyr Lys Leu Arg Gln Lys  
20 25

CCC GGG GAG GGC CCA GCA GCT GAC CCG  
Pro Gly Glu Gly Pro Ala Ala Asp Pro  
35 40

GCT GGA GAT GAG TTC GAG ACC CGC TTC  
Ala Gly Asp Glu Phe Glu Thr Arg Phe  
50 55

GCG GCT CAG CTG CAT GTG ACC CCA GGC  
Ala Ala Gln Leu His Val Thr Pro Gly  
65 70

CAG GTC TCC GAC GAA CTT TTT CAA GGG  
Gln Val Ser Asp Glu Leu Phe Gln Gly  
85

GTA GCC TTC TTT CTC TTT GGG GCT GCA  
Val Ala Phe Phe Leu Phe Gly Ala Ala  
100 105

*Fig. 9A (i)*

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[illegible]

**Fig. 9A ( ii )**  
**SUBSTITUTE SHEET (RULE 26)**

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AAG GAG ATG GAA CCA CTG GTG GGA CAA  
 Lys Glu Met Glu Pro Leu Val Gly Gln  
 115 120

TAC CTG GAG ACG CGG CTG GTC GAC TGG  
 Tyr Leu Glu Thr Arg Leu Val Asp Trp  
 130 135

GCG GAG TTC ACA GCT CTA TAC GGG GAC  
 Ala Glu Phe Thr Ala Leu Tyr Gly Asp  
 145 150

CGT CTG CGG GAG GGG AAC TGG GCA TCA  
 Arg Leu Arg Glu Gly Asn Trp Ala Ser  
 165

GCC GTG GCA CTG GGG GCC CTG GTA ACT  
 Ala Val Ala Leu Gly Ala Leu Val Thr  
 180 185

AAG TGA A  
 Lys \*

Fig. 9A ( iii )

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- 21/26

GTG CAG GAG TGG ATG GTG GCC	384
Val Gln Glu Trp Met Val Ala	
125	
ATC CAC AGC AGT GGG GGC TGG	432
Ile His Ser Ser Gly Gly Trp	
140	
GGG GCC CTG GAG GAG GCG CGG	480
Gly Ala Leu Glu Glu Ala Arg	
155 160	
GTG AGG ACA GTG CTG ACG GGG	528
Val Arg Thr Val Leu Thr Gly	
170 175	
GTA GGG GCC TTT TTT GCT AGC	576
Val Gly Ala Phe Phe Ala Ser	
190	
	583

Fig. 9A ( iv )

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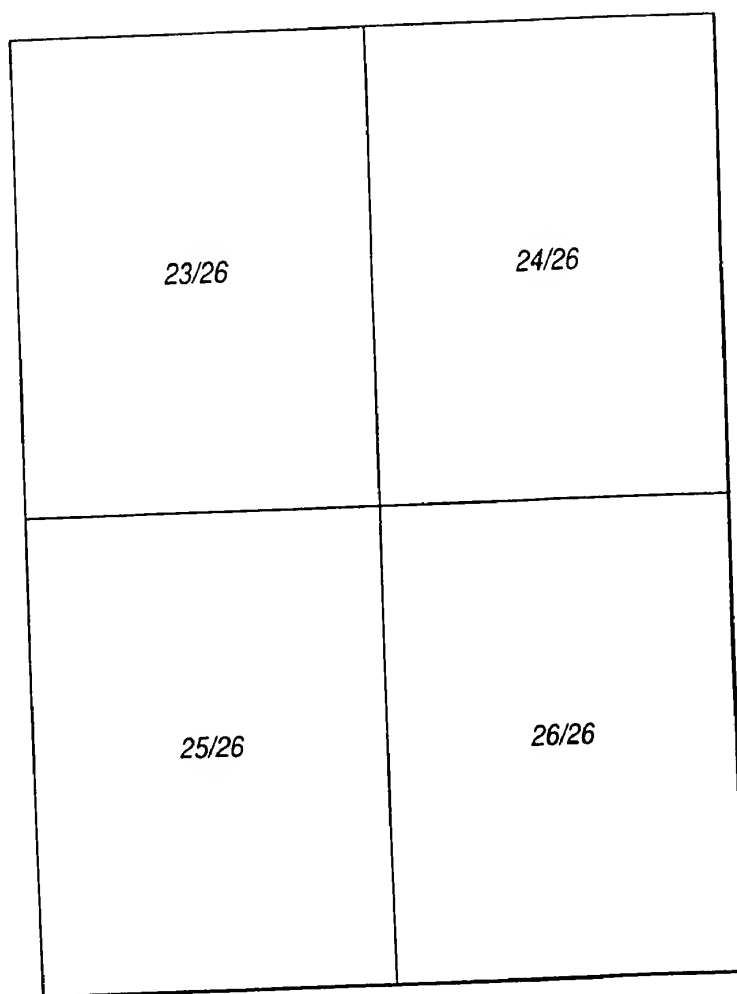


Fig. 9B

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ATG CCG ACC CCA GCC TCA ACC CCA GAC  
Met Pro Thr Pro Ala Ser Thr Pro Asp  
1 5

TTT GTA GGC TAT AGG CTG AGG CAG AAG  
Phe Val Gly Tyr Arg Leu Arg Gln Lys  
20 25

CCT GGG GAA GGC CCA GCC GCC GAC CCG  
Pro Gly Glu Gly Pro Ala Ala Asp Pro  
35 40

GCT GGA GAC GAG TTT GAG ACC CGT TTC  
Ala Gly Asp Glu Phe Glu Thr Arg Phe  
50 55

GCC GCT CAG CTG CAC GTG ACC CCA GGC  
Ala Ala Gln Leu His Val Thr Pro Gly  
65 70

CAG GTT TCC GAC GAA CTT TTC CAA GGG  
Gln Val Ser Asp Glu Leu Phe Gln Gly  
85

GTG GCA TTC TTT GTC TTT GGG GCT GCC  
Val Ala Phe Phe Val Phe Gly Ala Ala  
100 105

Fig. 9B (i)

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ACA CGC GCT CTA GTG GCT GAC	48
Thr Arg Ala Leu Val Ala Asp	
10 15	
GGT TAT GTC TGT GGA GCT GGG	96
Gly Tyr Val Cys Gly Ala Gly	
30	
CTG CAC CAA GCC ATG CGG GCT	144
Leu His Gln Ala Met Arg Ala	
45	
CGC CGC ACC TTC TCT GAC CTG	192
Arg Arg Thr Phe Ser Asp Leu	
60	
TCA GCC CAG CAA CGC TTC ACC	240
Ser Ala Gln Gln Arg Phe Thr	
75 80	
GGC CCT AAC TGG GGC CGT CTT	288
Gly Pro Asn Trp Gly Arg Leu	
90 95	
CTG TGT GCT GAG AGT GTC AAC	336
Leu Cys Ala Glu Ser Val Asn	
110	

Fig. 9B (ii)

SUBSTITUTE SHEET (RULE 26)



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AAA GAA ATG GAG CCT TTG GTG GGA CAA  
 Lys Glu Met Glu Pro Leu Val Gly Gln  
 115 120

TAC CTG GAG ACA CGT CTG GTC GAC TGG  
 Tyr Leu Glu Thr Arg Leu Ala Asp Trp  
 130 135

GCG GAC TTC ACA GCT CTA TAC GGG GAC  
 Ala Asp Phe Thr Ala Leu Tyr Gly Asp  
 145 150

CGT CTG CGG GAG GGC AAC TGG GCA TGA  
 Arg Leu Arg Glu Gly Asn Trp Ala \*  
 165

GCC GTG GCA CTG GGG GCC CTG GTA ACT  
 Ala Val Ala Leu Gly Ala Leu Val Thr  
 180 185

AAG TG  
 Lys

Fig. 9B ( iii )

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- 26/26

GTC	CAG	GAT	TGG	ATC	GTG	GCC	384
Val	Gln	Asp	Trp	Ile	Val	Ala	
			125				
ATC	CAC	AGC	AGT	GGC	GGC	TGG	432
Ile	His	Ser	Ser	Gly	Gly	Trp	
			140				
GGG	GCC	CTG	GAG	GAC	GCA	CGG	480
Gly	Ala	Leu	Glu	Asp	Ala	Arg	
		155				160	
GTG	AGC	ACA	GTG	GTG	ACG	GGG	528
Val	Ser	Thr	Val	Val	Thr	Gly	
			170			175	
GTA	GGG	GCC	TTT	TTT	GCT	AGC	576
Val	Gly	Ala	Phe	Phe	Ala	Ser	
			190				
							582

Fig. 9B ( iv )

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atg gcg acc cca gcc tca acc cca gac aca cgg gct cta gtg gct gac 48  
 Met Ala Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp  
 1 5 10 15

ttt gta ggc tat agg ctg agg cag aag ggt tat gtc tgt gga gct ggc 96  
 Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly  
 20 25 30

cct ggg gaa ggc cca gcc gcc gac ccg ctg cac caa gcc atg cgg gct 144  
 Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala  
 35 40 45

gct gga gac gag ttt gag acc cgt ttc cgc cgc acc ttc tct gac ctg 192  
 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu  
 50 55 60

gcc gct cag cta cac gtg acc cca ggc tca gcc cag caa cgc ttc acc 240  
 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr  
 65 70 75 80

cag gtt tcc gac gaa ctt ttc caa ggg ggc cct aac tgg ggc cgt ctt 288  
 Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu  
 85 90 95

gtg gca ttc ttt gtc ttt ggg gct gcc ctg tgt gct gag agt gtc aac 336  
 Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn  
 100 105 110

aaa gaa atg gag cct ttg gtg gga caa gtg cag gat tgg atg gtg gcc 384  
 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Met Val Ala  
 115 120 125

tac ctg gag aca cgt ctg gct gac tgg atc cac agc agt ggc ggc tgg 432  
 Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp  
 130 135 140

gcg gag ttc aca gct cta tac ggg gac ggg gcc ctg gag gag gca cgg 480  
 Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg  
 145 150 155 160

cgt ctg cgg gag ggg aac tgg gca tca gtg agg aca gtg ctg acg ggg 528  
 Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly  
 165 170 175

gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ttt ttt gct agc 576  
 Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser  
 180 185 190

aag tga 582  
 Lys

Figure 9B

	A	S1			
Bclw	MATPAST	DT KALVADFVGY KLRQKGY	VCG	AGPGEGPAAD	PLHQAMRAAG 5 0
Bclw-Rox	MATPAST	DT RALVADFVGY KLRQKGY	VCG	AGPGEGPAAD	PLHQAMRAAG 5 0

			S2		
Bclw	DEFETRFRRT	FSDLAAQLHV	TPGSAQQ	FT QVSDELFGGG	PNWGRLVAFF 1 0 0
Bclw-Rox	DEFETRFRRT	FSDLAAQLHV	TPGSAQQ	FT QVSDELFGGG	PNWGRLVAFF 1 0 0

			E		S3	
Bclw	VFGA	ALCAES	VNKEMEPLVG	QVQDWMVAYL	ETRLAD	WIHS SGGWAEFTAL 1 5 0
Bclw-Rox	VFGA	ALCAES	VNKEMEPLVG	QVQDWMVAYL	ETRLAD	WIHS SGGWAEFTAL 1 5 0

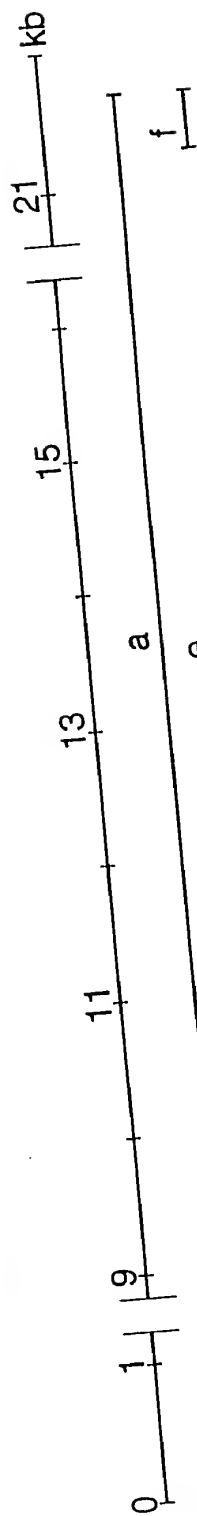
Bclw	YGD	GALEEAR	RLREGNWASV	RTVLTGAVAL	GALVTVGAF	ASK* 1 9 3
Bclw-Rox	ARVREMEEEA	EKLKELQNEV	EKQMNMSPPP	GNAGPVIMSL	EKMEADARS	2 0 0

Bclw-Rox	IYVGNVDYGA	TAELEAHFH	GCGSVNRVTI	LCDKFSGHPK	GFAYIEFS	SDK 2 5 0

Bclw-Rox	ESVRTSLALD	ESLFRGRQIK	VIPKRTNRPG	ISTTDRGFPR	SRYRARTTNY	3 0 0

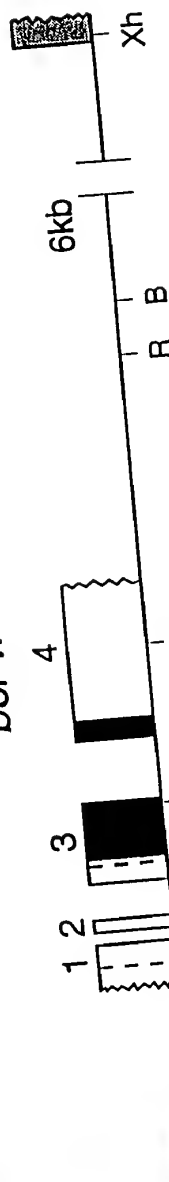
Bclw-Rox	NSSRSRFYSG	FNSRPRGRIY	RGRARATSWY	SPY*		3 3 3

# Genetic map

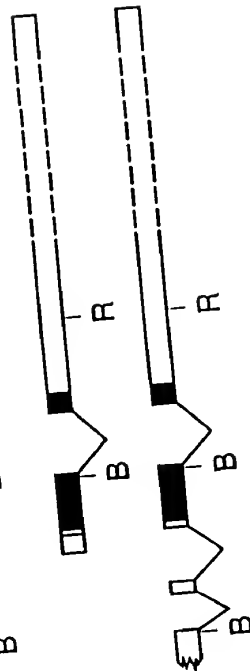


rox

bcl-w



bcl-w



bcl-w-rox

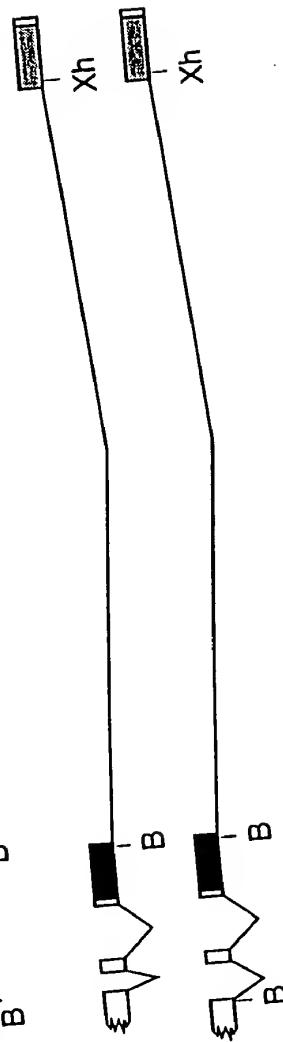


FIGURE 2

3.7 →

J774  
P388D1  
RAW 309Cr  
RAW 264.7  
3MES/RAF  
LYH7  
BAF3  
W274  
W265  
W3BD-  
FDC-P1  
FD/Bcl-2  
416B  
W112.1  
W105.7  
EL4.1  
YAC1  
W404.1  
ABLS8.1

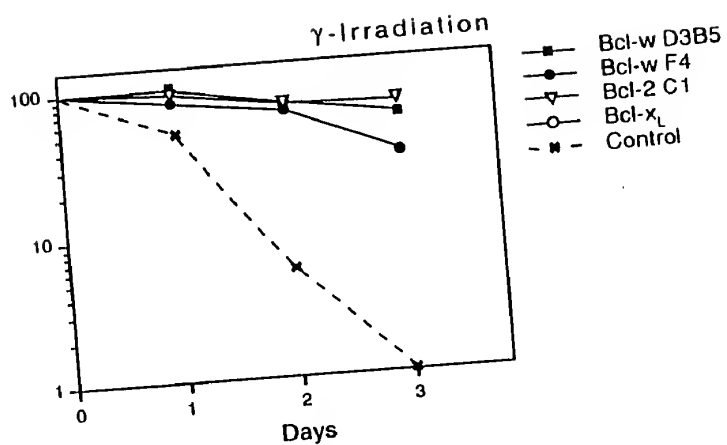
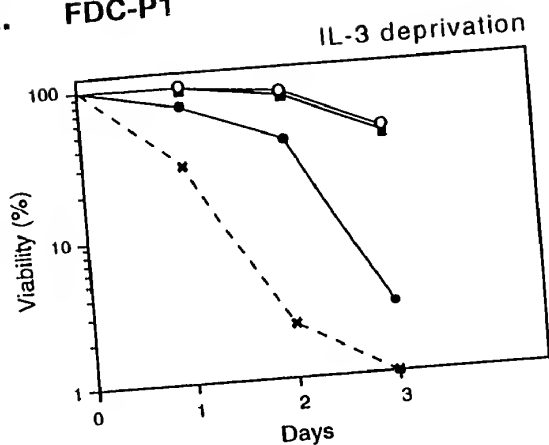
m0  
myeloid

FIGURE 3



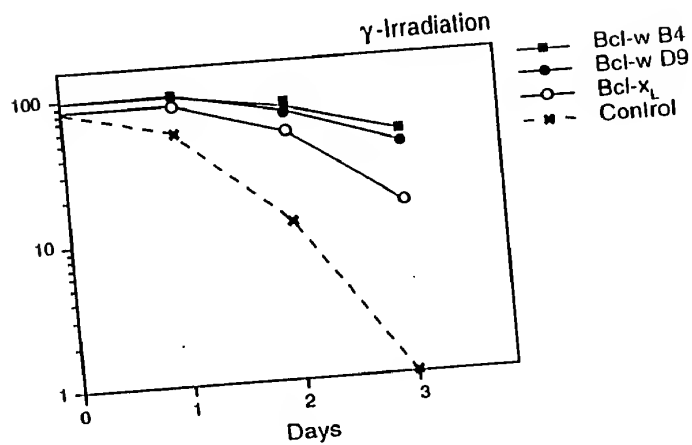
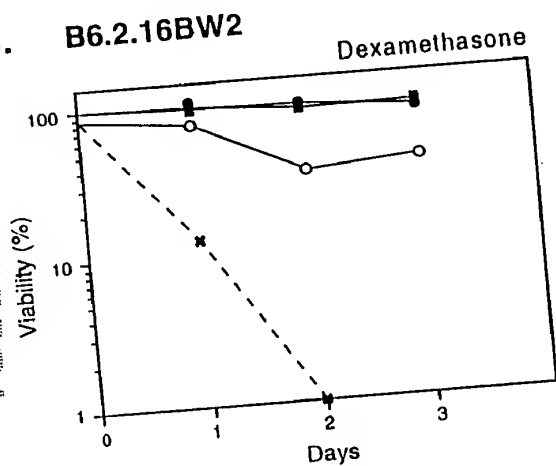


**A. FDC-P1**



**B.**

**B.**



C. CH1

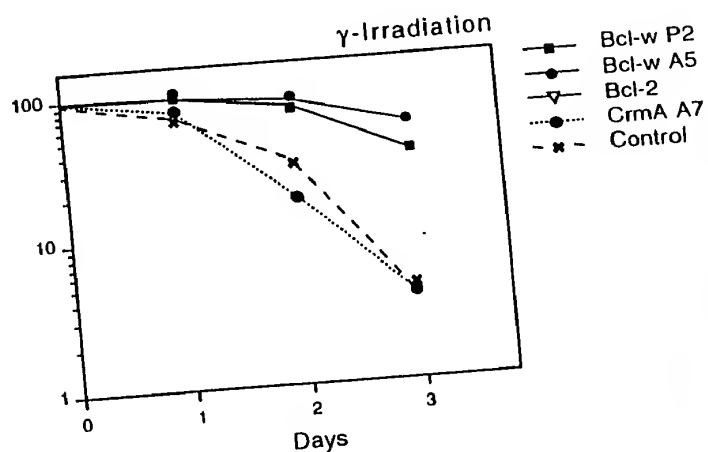
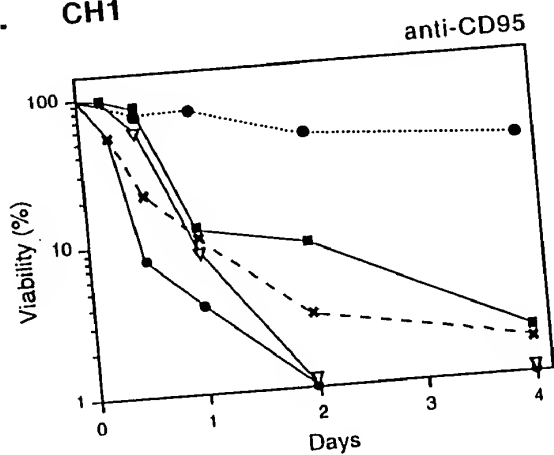


FIGURE 5

Figure 1 shows a schematic representation of the four genes (Sftp1, Tcra, Bclw, Gja3) and their four alleles. Each gene is represented by a 2x2 grid of squares. Black squares indicate the presence of a restriction site, and white squares indicate its absence. The alleles are numbered 59, 62, 3, 8, 0, 1, 1, 0 from left to right.

Gene	Allele 59	Allele 62	Allele 3	Allele 8	Allele 0	Allele 1	Allele 1	Allele 0
Sftp1	Black	White	White	Black	White	Black	White	Black
Tcra	Black	White	Black	White	White	Black	White	Black
Bclw	Black	White	Black	White	Black	White	White	Black
Gja3	Black	White	Black	White	Black	White	Black	White

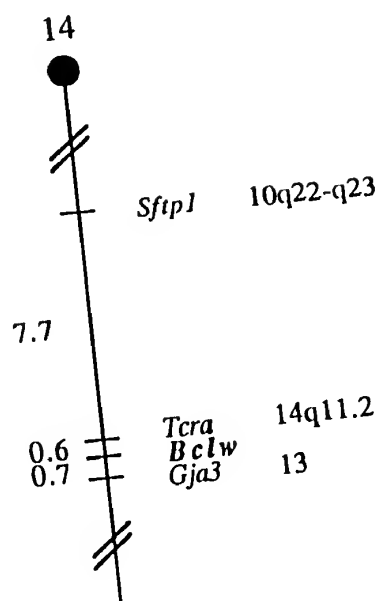


FIGURE 6

FOOD RESIDUE

I



FIGURE 7

[illegible]

Bcl2	SQPGHTPHTA	ASRDPVARTS	PLQTPAAPGA	AAGPAL....	...SPVPBVV	93
Bclx	METPSAINGN	PSWH.LADSP	AVNGATGHSS	SLDARE....	...VIPMAAV	86
Bclw	.....	.....	.....	.....	...GPAADPL	42
Bak	EQVAQDTEE	FRSYVFYRHQ	QEQAEGVAA	PADPEVTL	LQPSSTMGQV	74
Bax	MKTG.....	ALLQG	FIDRAGRMG	GEAPALDE	VPQDASTKKL	59

S2

BH1

Bax MKTG .....  
 BH3 NH1 S2 BH1  
 BC12 HLTLPQAGDE FSRRYRDFFA FMSRQHLITZ FTARGREATV VEELFRDG.V 142  
 BC1X KQALFEAGDE FELRYRFAFS DLTSQLHITP GTAYQSFEQV VNELFRDG.V 135  
 BC1W HQAMEAAGDE FETEFRETES DLAAQLHITP GSAQQRFQV SCELEQGS.P 91  
 BAK GROLAILEGDD INRRYDSEFO TMLQHLQPTA ENAYEYETXI TSLEESG.I 123  
 Bax SECKRIGDE LDS..NMELQ RMIAAVD..T DSPREVEFRV AADMFSDBGF 105  
 Bik TACEGDE MD  
 Δ Δ Δ Δ S3 BH12

Bc12 WNGPIVAFHE FGQVMEVESV NRFMSPLVDN IALWHTETYN RH.LHTWIQD 191  
 Bc1x1 NWCRIVAFFS FGGALCVESV DKEMQVLUSR IAAMMATYN DH.LEEWIQE 184  
 Bclw NHGHVAFV FGAALCASSV NKEMEPVUGQ VQEMNVAVIE TR.LADWHS 140  
 Bak WNGHIVAFHE FGYRLATHVY QHGLTGFLGQ VTRFVVDL HHCIARWIAQ 173  
 Bax NWGRVAFV FASKEVLKAL CTKVPRELRT IMGWTLDEER ERLLG.WIQD 154

Bcl2	NGGNDATFVEL	YG	....PSMRPL	FDFS\WLSLRT	LLSLAL.VGA	CITLHAYLGH	K....	239
BclxL	NEGWDTFVEL	YG	....NNAAAE	SRKGQERFNR	WFLTGMTVAG	VVLDSLFSR	K....	233
Bclw	SEGWAFTTA	YG	GDGALEEARRL	REGNWASVRT	VLGVAALGA	LUTVSAFFAS	K....	193
Bak	RGGWVAALNL	GN	.....	.....	G.FILNVLDVVLG	VVILGQFVVR	FFFKS	211
Bax	QGGWDGLLSY	FG	.....	.....	TP.TWQTVTIEVA	GVLTA\SLTIW	KKMG.	192

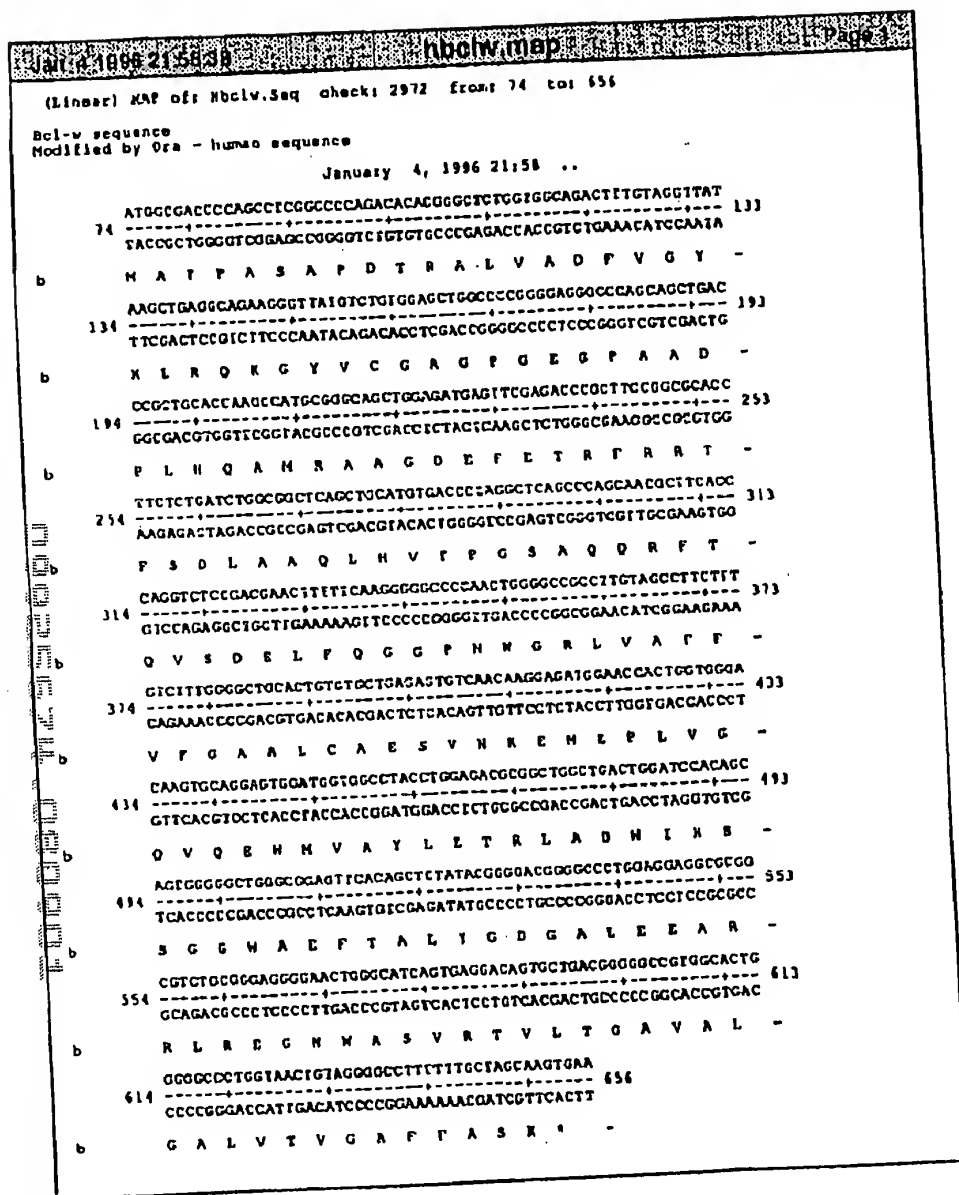


FIGURE 9A

